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(54) MODULATEURS SELECTIFS DU RECEPTEUR .GAMMA.
ACTIVE DE LA PROLIFERATION DES PEROXYSOMES ET
TECHNIQUES D'UTILISATIONS CORRESPONDANTES
(54) SELECTIVE MODULATORS OF PEROXISOME
PROLIFERATOR ACTIVATED RECEPTOR-.GAMMA., AND
METHODS FOR THE USE THEREOF

(57) Dans le cadre de cette invention, il est présenté une classe de composés capables moduler de manière sélective des processus régulés par un récepteur gamma activé de la prolifération des peroxysomes (PPAR-gamma.). L'identification de ces composés permet d'intervenir de manière sélective dans des voies régulées par PPAR-gamma, sans entraîner des effets intempestifs sur des voies régulées par d'autres isoformes de PPAR.

(57) In accordance with the present invention, there are provided a class of compounds which are capable of selectively modulating processes mediated by peroxisome proliferator activated receptor-gamma (PPAR-gamma.). The identification of such compounds makes possible the selective intervention in PPAR-gamma mediated pathways, without exerting inadvertent effects on pathways mediated by other PPAR isoforms.

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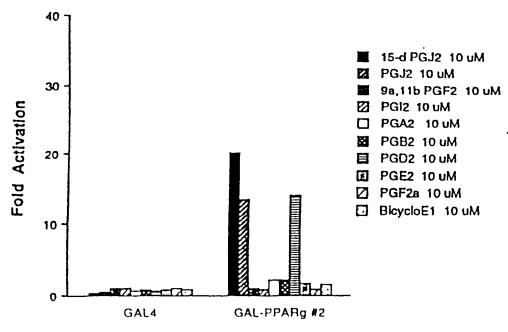
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(54) Title: SELECTIVE MODULATORS OF PEROXISO	ME PR	OLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS

(54) Title: SELECTIVE MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF



(57) Abstract

In accordance with the present invention, there are provided a class of compounds which are capable of selectively modulating processes mediated by peroxisome proliferator activated receptor-gamma (PPAR γ). The identification of such compounds makes possible the selective intervention in PPAR γ mediated pathways, without exerting inadvertent effects on pathways mediated by other PPAR isoforms.

Selective Modulators of Peroxisome Proliferator

Activated Receptor-gamma, and Methods for the Use Thereof

FIELD OF THE INVENTION

The present invention relates to methods for the modulation of nuclear receptor mediated processes.

In a particular aspect, the present invention relates to the use of a specific class of compounds for the modulation of processes mediated by peroxisome proliferator activated receptor-gamma (PPAR-y). In another aspect, the present invention relates to methods of testing compounds for their ability to regulate transcription-activating effects of PPAR-y.

BACKGROUND OF THE INVENTION

Peroxisome proliferators are a structurally diverse group of compounds which, when administered to rodents, elicit dramatic increases in the size and number 15 of hepatic and renal peroxisomes, as well as concomitant increases in the capacity of peroxisomes to metabolize fatty acids via increased expression of the enzymes required for the B-oxidation cycle (Lazarow and Fujiki, Ann. Rev. Cell Biol. 1:489-530 (1985); Vamecq and Draye, 20 Essays Biochem. 24:1115-225 (1989); and Nelali et al., Cancer Res. 48:5316-5324 (1988)). Chemicals included in this group are the fibrate class of hypolipidermic drugs, herbicides, and phthalate plasticizers (Reddy and Lalwani, Crit. Rev. Toxicol. 12:1-58 (1983)). Peroxisome 25 proliferation can also be elicited by dietary or physiological factors such as a high-fat diet and cold acclimatization.

Insight into the mechanism whereby peroxisome proliferators exert their pleiotropic effects was provided by the identification of a member of the nuclear hormone receptor superfamily activated by these chemicals (Isseman and Green, Nature 347-645-650 (1990)). receptor, termed peroxisome proliferator activated receptor alpha (PPARa), was subsequently shown to be activated by a variety of medium and long-chain fatty acids and to stimulate expression of the genes encoding 10 rat acyl-CoA oxidase and hydratase-dehydrogenase (enzymes required for peroxisomal B-oxidation), as well as rabbit cytochrome P450 4A6, a fatty acid w-hydroxylase (Gottlicher et al., Proc. Natl. Acad. Sci. USA 89:4653-4657 (1992); Tugwood et al., EMBO J. 11:433-439 (1992); 15 Bardot et al., Biochem. Biophys. Res. Comm. 192:37-45 (1993); Muerhoff et al., J. Biol. Chem. 267:19051-19053 (1992); and Marcus et al., Proc. Natl. Acad. Sci. USA 90(12):5723-5727 (1993).

The above-noted references suggest a 20 physiological role for PPARα in the regulation of lipid metabolism. PPARa activates transcription by binding to DNA sequence elements, termed peroxisome proliferator response elements (PPRE), as a heterodimer with the retinoid X receptor. The retinoid X receptor is 25 activated by 9-cis retinoic acid (see Kliewer et al., Nature 358:771-774 (1992), Gearing et al., Proc. Natl. Acad. Sci. USA 90:1440-1444 (1993), Keller et al., Proc. Natl. Acad. Sci. USA 90:2160-2164 (1993), Heyman et al., Cell 68:397-406 (1992), and Levin et al., Nature 355:359-30 361 (1992)). Since the PPARa-RXR complex can be activated by peroxisome proliferators and/or 9-cis retinoic acid, the retinoid and fatty acid signaling pathways are seen to converge in modulating lipid metabolism.

Since the discovery of PPARa, additional isoforms of PPAR have been identified, e.g., PPARB, PPARB and PPARB, which are spatially differentially expressed. Because there are several isoforms of PPAR, it would be desirable to identify compounds which are capable of selectively interacting with only one of the PPAR isoforms. Such compounds would find a wide variety of uses, such as, for example, in the prevention of obesity, for the treatment of diabetes, and the like.

BRIEF DESCRIPTION OF THE INVENTION

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In accordance with the present invention, we have identified a class of compounds which are capable of selectively modulating processes mediated by peroxisome proliferator activated receptor-gamma (PPAR-y). The identification of such compounds makes possible the selective intervention in PPAR-y mediated pathways, without exerting inadvertent effects on pathways mediated by other PPAR isoforms.

BRIEF DESCRIPTION OF THE FIGURES

20 Figure 1 illustrates the activation of a GAL4-PPARy fusion protein by a variety of prostaglandin or prostaglandin-like compounds. In the figure, black bars represent 15-deoxy- $\Delta^{12,14}$ -prostaglandin- J_2 (15-d PGJ2), the dark, striped bars represent prostaglandin-J2 (PGJ2), the darkly shaded bars represent 9α , 11β -prostaglandin-F, (9a,11bPGF2), the light, closely (diagonally) striped bars represent prostaglandin-I2 (PGI2), the open bars represent prostaglandin-A, (PGA2), the dark bars with light dots represent prostaglandin-B, (PGB2), the 30 horizontally hatched bars represent prostaglandin-D, (PGD2), the light bars with dark dots represent prostaglandin-E2 (PGE2), the light, sparsely (diagonally) hatched bars represent prostaglandin-F2a (PGF2a), and the

light bars with sparsely spaced dots represent bicycloprostaglandin-E, (BicycloE1).

Figure 2 illustrates the dose response for activation of a GAL4-PPARy fusion protein by a variety of 5 prostaglandin or prostaglandin-like compounds. figure, open circles represent prostaglandin-D2 (PGD2), darkened circles represent prostaglandin-J2 (PGJ2), open squares represent Δ^{12} -prostaglandin-J $_2$ (Δ 12-PGJ2), and darkened squares represent 15-deoxy- $\Delta^{12,14}$ -prostaglandin-J, $(15-\text{deoxy}-\Delta 12,14-\text{PGJ2})$.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, there are provided methods for modulating process(es) mediated by peroxisome proliferator activated receptor-gamma 15 (PPAR-y), said method comprising conducting said process(es) in the presence of at least one PPAR-yselective prostaglandin or prostaglandin-like compound or precursor thereof.

PPAR-y-selective prostaglandins or 20 prostaglandin-like compounds contemplated for use in the practice of the present invention include members of the prostaglandin-J, family of compounds (e.g., prostaglandin- J_2 , Δ^{12} -prostaglandin- J_2 or 15-deoxy- $\Delta^{12,14}$ -prostaglandin- J_2), members of the 25 prostaglandin- D_2 family of compounds (e.g., prostaglandin-D,), or precursors thereof, as well as compounds having the structure I:

WO 96/33724 PCT/US96/05465

wherein:

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A is selected from hydrogen or a leaving group
at the α- or β- position of the ring, or A
is absent when there is a double bond
between C^α and C^β of the ring;

X is an alkyl, substituted alkyl, alkenyl,
substituted alkenyl, alkynyl or
substituted alkynyl group having in the
range of 2 up to 15 carbon atoms; and
Y is an alkyl, substituted alkyl, alkenyl,
substituted alkenyl, alkynyl or
substituted alkynyl group having in the
range of 2 up to 15 carbon atoms.

As employed herein, the term "leaving group" refers to functional groups which can readily be removed from the precursor compound, for example, by nucleophilic displacement, under E₂ elimination conditions, and the like. Examples include hydroxy groups, alkoxy groups, tosylates, brosylates, halogens, and the like.

As employed herein, "lower alkyl" refers to straight or branched chain alkyl groups having in the range of about 1 up to 4 carbon atoms; "alkyl" refers to straight or branched chain alkyl groups having in the range of about 1 up to 12 carbon atoms; "substituted alkyl" refers to alkyl groups further bearing one or more substituents such as hydroxy, alkoxy (of a lower alkyl group), mercapto (of a lower alkyl group), halogen,

trifluoromethyl, cyano, nitro, amino, carboxyl, carbamate, sulfonyl, sulfonamide, and the like.

As employed herein, "cycloalkyl" refers to cyclic ring-containing groups containing in the range of about 3 up to 8 carbon atoms, and "substituted cycloalkyl" refers to cycloalkyl groups further bearing one or more substituents as set forth above.

As employed herein, "alkenyl" refers to straight or branched chain hydrocarbyl groups having at least one carbon-carbon double bond, and having in the range of about 2 up to 12 carbon atoms and "substituted alkenyl" refers to alkenyl groups further bearing one or more substituents as set forth above.

As employed herein, "alkynyl" refers to

15 straight or branched chain hydrocarbyl groups having at
least one carbon-carbon triple bond, and having in the
range of about 2 up to 12 carbon atoms, and "substituted
alkynyl" refers to alkynyl groups further bearing one or
more substituents as set forth above.

As employed herein, "aryl" refers to aromatic groups having in the range of 6 up to 14 carbon atoms and "substituted aryl" refers to aryl groups further bearing one or more substituents as set forth above.

As employed herein, "alkylaryl" refers to
25 alkyl-substituted aryl groups and "substituted alkylaryl"
refers to alkylaryl groups further bearing one or more
substituents as set forth above.

As employed herein, "arylalkyl" refers to aryl-substituted alkyl groups and "substituted arylalkyl"

30 refers to arylalkyl groups further bearing one or more substituents as set forth above.

As employed herein, "arylalkenyl" refers to aryl-substituted alkenyl groups and "substituted arylalkenyl" refers to arylalkenyl groups further bearing one or more substituents as set forth above.

As employed herein, "arylalkynyl" refers to aryl-substituted alkynyl groups and "substituted arylalkynyl" refers to arylalkynyl groups further bearing one or more substituents as set forth above.

As employed herein, "aroyl" refers to aryl10 carbonyl species such as benzoyl and "substituted aroyl"
refers to aroyl groups further bearing one or more
substituents as set forth above.

As employed herein, "heterocyclic" refers to cyclic (i.e., ring-containing) groups containing one or more heteroatoms (e.g., N, O, S, or the like) as part of the ring structure, and having in the range of 3 up to 14 carbon atoms and "substituted heterocyclic" refers to heterocyclic groups further bearing one or more substituents as set forth above.

As employed herein, "acyl" refers to alkylcarbonyl species.

As employed herein, "halogen" or "halo" refers to fluoro substituents, chloro substituents, bromo substituents or iodo substituents.

In a presently preferred aspect of the present invention, "X" of Formula I is selected from:

$$-(CRR)_m-Z$$
,

$$-(CRR)_{m'}-C(R)=C(R)-(CRR)_{m'}-Z$$
, or

-(CRR)_{m"}-C
$$\equiv$$
C-(CRR)_{m"}-Z, wherein:

each R is independently selected from H, lower alkyl, substituted lower alkyl,

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hydroxy, lower alkoxy, thioalkyl,
halogen, trifluoromethyl, cyano,
nitro, amino, carboxyl, carbamate,
sulfonyl or sulfonamide,

m falls in the range of 1 up to 15,
each m' falls independently in the range
of 0 up to 12, with the proviso that
the total chain length of the alkenyl
moiety does not exceed 15 carbon
atoms,
each m" falls independently in the range
of 0 up to 12, with the proviso that
the total chain length of the alkynyl
moiety does not exceed 15 carbon
atoms, and

Z is a polar, heteroatom-containing
 substituent.

Those of skill in the art can readily identify numerous groups which satisfy the requirement that Z be a 20 polar, heteroatom-containing (i.e., O, N, S, or the like) substituent. Thus, Z can be selected from cyano, nitro, amino, carbamate, or a substituent having the structure:

-CH₂OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl, aryl, or the like;

-C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted aryl, aryloxy, arylamino, alkylaryl, substituted alkylaryl, arylalkyl, substituted alkylaryl, heterocyclic, substituted arylalkyl, heterocyclic or trifluoromethyl,

-CO₂R''', wherein R''' is selected from H, alkyl, alkenyl, alkynyl, or the like;

-SR', -S(0)R', -S(0)₂R' or -S(0)₂NHR', wherein each R' is as defined above, and the like.

Especially preferred compounds employed in the practice of the present invention are those wherein "X" of Formula I is

-CRR-C(R)=C(R)-(CRR)_m-Z, wherein:

each R is independently selected from H,

lower alkyl, substituted lower alkyl,

hydroxy, alkoxy (of a lower alkyl

group), halogen, trifluoromethyl,

amino, carboxyl or sulfonyl,

m falls in the range of 1 up to 6, and

Z is selected from -CH₂OH, -CH₂OAc, -CO₂H,

-CO₂Me or -CO₂Et.

In another preferred aspect of the present invention, "Y" of Formula I is selected from:

 $= C(R) - [C(R) = C(R)]_{n} - (CRR)_{n'} - Z' \quad (II),$ $= C(R) - [C = C]_{n} - (CRR)_{n'} - Z' \quad (IIA),$ $= C(R) - CRR - CR(R') - (CRR)_{n'} - Z' \quad (III),$ $- [C(R) = C(R)]_{n} - (CRR)_{n'} - Z' \quad (IV), \text{ or }$ $- [C = C]_{n} - (CRR)_{n'} - Z' \quad (IVA),$ wherein

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each R is independently as defined
 above,

each R' is independently selected from H, lower alkyl, substituted lower alkyl or a leaving group,

Z' is selected from H, lower alkyl or substituted lower alkyl,

n falls in the range of 0 up to 4, n' falls in the range of 2 up to 12, and n" falls in the range of 1 up to 3.

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Especially preferred compounds contemplated for use in the practice of the present invention include those wherein "Y" of Formula I is selected from:

each R' is independently as defined above,

Z' is selected from H, lower alkyl or substituted lower alkyl, and n' falls in the range of 1 up to 6.

Presently most preferred compounds for use in
the practice of the present invention include those
wherein "Y" of Formula I is

$$=C(R)-C(R)=C(R)-(CRR)_{n'}-Z'$$
 (II),

wherein each R is selected from H, lower alkyl or substituted lower alkyl, n is 1, n' falls in the range of 20 about 2 up to 6, and Z' is selected from H or lower alkyl; or those wherein "Y" of Formula I is

$$=C(R)-CRR-CR(R')-(CRR)_{n'}-Z' (III) or \\ -C(R)=C(R)-CR(R')-(CRR)_{n'}-Z' (IV),$$

wherein each R is selected from H, lower alkyl or

substituted lower alkyl, R' is selected from H, lower
alkyl, or an hydroxy group, n is 1, n' falls in the range
of about 2 up to 6, and Z' is selected from H or lower
alkyl.

Referring to the structural formulae set forth

30 above, prostaglandin-D₂ (Pg-D2) is described by Formula I

(as set forth above), wherein A is 9-OH, Y is IV, each R

is hydrogen, R' is hydroxy, Z is -CO₂H, m is 3, Z' is

methyl, n is 1 and n' is 4; prostaglandin-J₂ (Pg-J2) is

described by Formula I, wherein A is absent, Y is IV,

35 each R is hydrogen, R' is hydroxy, Z is -CO₂H, m is 3, Z'

is methyl, n is 1 and n' is 4; Δ^{12} -prostaglandin-J₂ (Δ^{12} -Pg-J2) is described by Formula I, wherein A is absent, Y is III, each R is hydrogen, R' is hydroxy, Z is -CO₂H, m is 3, Z' is methyl, n is 1 and n' is 4; 15-deoxy- $\Delta^{12,14}$ -prostaglandin-J₂ (15-deoxy- $\Delta^{12,14}$ -Pg-J2) is described by Formula I, wherein A is absent, Y is II, each R is hydrogen, Z is -CO₂H, m is 3, Z' is methyl, n is 1 and n' is 4.

The above-described compounds can be readily

or prepared using a variety of synthetic methods, as are
well known by those of skill in the art. For example,
many of the above-described compounds can be prepared
chemically or enzymatically, from the naturally occurring
precursor, arachidonic acid.

As employed herein, the term "modulate" refers
to the ability of a modulator for a member of the
steroid/thyroid superfamily to either directly (by
binding to the receptor as a ligand) or indirectly (as a
precursor for a ligand or an inducer which promotes
production of ligand from a precursor) induce expression
of gene(s) maintained under hormone expression control,
or to repress expression of gene(s) maintained under such
control.

As employed herein, the phrase "processes

25 mediated by PPARy" refers to biological, physiological,
endocrinological, and other bodily processes which are
mediated by receptor or receptor combinations which are
responsive to the PPAR-y-selective prostaglandin or
prostaglandin-like compounds described herein. Such

30 processes include cell differentiation to produce lipidaccumulating cells, modulation of blood glucose levels
and insulin sensitivity, regulation of leptin levels and
subsequent feeding levels (for the control of satiety
and/or appetite), regulation of thermogenesis and fatty

acid metabolism, regulation of fat levels for the treatment of lipodystrophies, control of cell differentiation for the treatment of myxoid liposarcomas, regulation of triglyceride levels and lipoproteins for the treatment of hyperlipidemia, modulation of genes expressed in adipose cells (e.g., leptin, lipoprotein, lipase, uncoupling protein, and the like), and the like.

In accordance with the present invention, modulation of processes mediated by PPARy can be

10 accomplished in vitro or in vivo. In vivo modulation can be carried out in a wide range of subjects, such as, for example, humans, rodents, sheep, pigs, cows, and the like.

ppar-y-selective prostaglandin or

prostaglandin-like compounds contemplated for use in the practice of the present invention can be employed for both in vitro and in vivo applications. For in vivo applications, the invention compounds can be incorporated into a pharmaceutically acceptable formulation for administration. Those of skill in the art can readily determine suitable dosage levels when compounds contemplated for use in the practice of the present invention are so used.

In accordance with another embodiment of the

25 present invention, there is provided a method of testing
compound(s) for the ability to regulate the
transcription-activating effects of a peroxisome
proliferator activated receptor-gamma (PPAR-y), said
method comprising assaying for changes in the level of

30 reporter protein present as a result of contacting cells
containing said receptor and reporter vector with said
compound;

wherein said reporter vector comprises:

PCT/US96/05465 WO 96/33724

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- a promoter that is operable in said (a)
- (b) a hormone response element, and
- a DNA segment encoding a reporter (c) protein,

wherein said reporter proteinencoding DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof.

Hormone response elements contemplated for use in the practice of the present invention are composed of at least one direct repeat of two or more half sites 15 separated by a spacer of one nucleotide. The spacer nucleotide can be selected from any one of A, C, G or T. Each half site of response elements contemplated for use in the practice of the invention comprises the sequence -RGBNNM-,

wherein

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R is selected from A or G; B is selected from G, C, or T; each N is independently selected from

A, T, C, or G; and

M is selected from A or C:

with the proviso that at least 4 nucleotides of said -RGBNNM- sequence are identical with the nucleotides at corresponding positions of the sequence -AGGTCA-.

30 Response elements employed in the practice of the present invention can optionally be preceded by N, wherein x falls in the range of 0 up to 5.

Presently preferred response elements contain at least one copy (with one, two or three copies most 35 common) of the minimal sequence:

AGGACA A AGGTCA (SEQ ID NO:4).

As noted above, the minimal sequence can optionally be flanked by additional residues, for example, as in the sequence:

5 GGACC AGGACA A AGGTCA CGTTC (SEQ ID NO:5).

In a preferred embodiment of the present invention, only the ligand binding domain of PPARy is utilized, in combination with the DNA binding domain of GAL4 protein, for the identification of PPARy ligands or ligand-precursors. This allows one to avoid possible background signal caused by the potential presence of endogenous PPARy in the host cells used for the assay.

The DNA binding domain of the yeast GAL4 protein comprises at least the first 74 amino acids

15 thereof (see, for example, Keegan et al., Science 231:699-704 (1986)). Preferably, the first 90 or more amino acids of the GAL4 protein will be used, with the first 147 amino acid residues of yeast GAL4 being presently most preferred.

20 The GAL4 fragment employed in the practice of the present invention can be incorporated into any of a number of sites within the PPARy receptor protein. example, the GAL4 DNA binding domain can be introduced at the amino terminus of the PPARy receptor protein, or the 25 GAL4 DNA binding domain can be substituted for the native DNA binding domain of the PPARy receptor, or the GAL4 DNA binding domain can be introduced at the carboxy terminus of the PPARy receptor protein, or at other positions as can readily be determined by those of skill in the art. 30 Thus, for example, a modified receptor protein can be prepared which consists essentially of amino acid residues 1-147 of GAL4, plus the ligand binding domain of PPARy (i.e., containing the ligand binding domain only of said receptor (i.e., residues 163-475 of SEQ ID NO:1),

substantially absent the DNA binding domain and amino terminal domain thereof).

Identification methods according to the present invention involve the use of a functional bioassay 5 system, wherein the modified receptor and a reporter plasmid are cultured in suitable host cells in the presence of test compound. Evidence of transcription (e.g., expression) of reporter gene is then monitored to determine the presence of an activated receptor-ligand 10 complex. Accordingly, the functional bioassay system utilizes two plasmids: an "expression" plasmid and a "reporter" plasmid. The expression plasmid can be any plasmid which contains and is capable of expressing DNA encoding the desired form of PPARy receptor protein 15 (i.e., intact receptor or GAL4 chimeric receptor as described hereinabove), in a suitable host cell. reporter plasmid can be any plasmid which contains an operative PPRE or GAL4 response element, as appropriate, functionally linked to an operative reporter gene.

20 Exemplary PPREs have been described in detail hereinabove. Exemplary GAL4 response elements are those containing the palindromic 17-mer:

5'-CGGAGGACTGTCCTCCG-3' (SEQ ID NO:6),

such as, for example, 17MX, as described by Webster et al., in Cell <u>52</u>:169-178 (1988), as well as derivatives thereof. Additional examples of suitable response elements include those described by Hollenberg and Evans in Cell <u>55</u>:899-906 (1988); or Webster et al. in Cell <u>54</u>:199-207 (1988).

30 Exemplary reporter genes include chloramphenical transferase (CAT), luciferase (LUC), beta-galactosidase (β -gal), and the like. Exemplary

promoters include the simian virus (SV) promoter or modified form thereof (e.g., ΔSV), the thymidine kinase (TK) premoter, the mammary tumor virus (MTV) promoter or modified form thereof (e.g., Δ MTV), and the like [see, 5 for example, Mangelsdorf et al., in Nature 345:224-229 (1990), Mangelsdorf et al., in Cell 66:555-561 (1991), and Berger et al., in J. Steroid Biochem. Molec. Biol. 41:733-738 (1992)]. The plasmids pGMCAT, pGHCAT, pTK- ${\rm GAL_p3\text{-}LUC}$, ${\rm \Delta MTV\text{-}GAL_p3\text{-}LUC}$, ${\rm \Delta MTV\text{-}GAL_p3\text{-}CAT}$, and the like, 10 are examples of reporter plasmids which contain an operative hormone responsive promoter/enhancer element functionally linked to an operative reporter gene, and can therefore be used in the above-described functional bioassay (see Example 2 for details on the preparation of 15 these plasmids). In pGMCAT, the operative hormone responsive promoter/enhancer element is the MTV LTR; in pGHCAT it is the functional portion of the growth hormone promoter. In both pGMCAT and GHCAT the operative reporter gene is the bacterial gene for chloramphenicol 20 acetyltransferase (CAT).

As used herein in the phrase "operative response element functionally linked to an operative reporter gene", the word "operative" means that the respective DNA sequences (represented by the terms

25 "PPRE," "GAL4 response element" and "reporter gene") are operational, i.e., work for their intended purposes; the word "functionally" means that after the two segments are linked, upon appropriate activation by a ligand-receptor complex, the reporter gene will be expressed as the

30 result of the fact that the "PPRE" or "GAL4 response element" was "turned on" or otherwise activated.

In practicing the above-described functional bioassay, the expression plasmid and the reporter plasmid are co-transfected into suitable host cells. The transfected host cells are then cultured in the presence

and absence of a test compound to determine if the test compound is able to produce activation of the promoter operatively linked to the PPRE or GAL4 response element of the reporter plasmid. Thereafter, the transfected and cultured host cells are monitored for induction (i.e., the presence) of the product of the reporter gene sequence.

Any cell line can be used as a suitable "host" for the functional bioassay contemplated for use in the practice of the present invention. Thus, in contrast to the requirements of prior art assay systems, when GAL4 chimerics are employed, there is no need to use receptor-negative cells in carrying out the invention process. Since the modified receptor employed in the practice of the present invention is the only species in the test cell which is capable of initiating transcription from a GAL4 response element, the expression of native receptor by the test cell does not contribute to background levels. Thus, the invention bioassay can be made to be very selective.

Cells contemplated for use in the practice of the present invention include transformed cells, nontransformed cells, neoplastic cells, primary cultures of different cell types, and the like. Exemplary cells 25 which can be employed in the practice of the present invention include Schneider cells, CV-1 cells, HuTu80 cells, F9 cells, NTERA2 cells, NB4 cells, HL-60 cells, 293 cells, Hela cells, yeast cells, and the like. Preferred host cells for use in the functional bioassay 30 system are COS cells and CV-1 cells. COS-1 (referred to as COS) cells are monkey kidney cells that express SV40 T antigen (Tag); while CV-1 cells do not express SV40 Tag. The presence of Tag in the COS-1 derivative lines allows the introduced expression plasmid to replicate and provides a relative increase in the amount of receptor 35

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produced during the assay period. CV-1 cells are presently preferred because they are particularly convenient for gene transfer studies and provide a sensitive and well-described host cell system.

The above-described cells (or fractions thereof) are maintained under physiological conditions when contacted with physiologically active compound.

"Physiological conditions" are readily understood by those of skill in the art to comprise an isotonic,
aqueous nutrient medium at a temperature of about 37°C.

In accordance with another embodiment of the present invention, there is provided a method of screening for antagonists of PPARy receptor proteins, said method comprising

15 culturing test cells containing

(i) increasing concentrations of at least one compound whose ability to inhibit the transcription activation activity of PPARy agonists is sought to be determined, and

(ii) optionally, at least one PPARy agonist,

wherein said test cells contain

(i) exogenous DNA which
expresses intact PPARy or a modified
form of PPARy, wherein the modified
form of PPARy contains the DNA
binding domain of GAL4, and

(ii) a PPRE or GAL4 response
element, respectively, operatively

(ii) a PPRE or GAL4 response
element, respectively, operatively
linked to a reporter gene; and
thereafter

19

assaying for evidence of transcription of said reporter gene in said cells as a function of the concentration of said compound in said culture medium, thereby indicating the ability of said compound to inhibit activation of transcription by PPARy agonists.

Media employed for such culturing may include agonist for the receptor being tested, or the receptor may be constitutive (i.e., not require the presence of agonist for activation), or a fixed concentration of agonist can be added to the media employed for such testing.

The above-described assays of the present invention have low background and a broad dynamic range.

In accordance with yet another embodiment of the present invention, there is provided a method for preventing obesity, said method comprising administering to a subject in need thereof an amount of a peroxisome proliferator activated receptor-gamma (PPAR-y) antagonist effective to block cell differentiation to produce lipid-accumulating cells.

As employed here, "obesity" refers generally to individuals who are at least about 20-30% over the average weight for his/her age, sex and height. Technically, "obese" is defined, for males, as individuals whose body mass index is greater than 27.8 kg/m^2 , and for females, as individuals whose body mass index is greater than 27.3 kg/m^2 .

Those of skill in the art recognize that there
30 are numerous cell types which are capable of
differentiation to produce "lipid-accumulating cells,"

such as, for example, mesenchymal cells (e.g., fibroblasts).

As employed herein, the phrase "amount... effective to block cell differentiation" refers to levels of compound sufficient to provide circulating concentrations high enough to effect activation of PPARy. Such a concentration typically falls in the range of about 10 nM up to 2 μ M; with concentrations in the range of about 100 nM up to 200 nM being preferred.

In accordance with a particular embodiment of the present invention, compositions comprising at least one prostaglandin or prostaglandin-like compound (as described above), and a pharmaceutically acceptable carrier are contemplated. Exemplary pharmaceutically acceptable carriers include carriers suitable for oral, intravenous, subcutaneous, intramuscular, intracutaneous, and the like administration. Administration in the form of creams, lotions, tablets, dispersible powders, granules, syrups, elixirs, sterile aqueous or non-aqueous solutions, suspensions or emulsions, and the like, is contemplated.

For the preparation of oral liquids, suitable carriers include emulsions, solutions, suspensions, syrups, and the like, optionally containing additives

25 such as wetting agents, emulsifying and suspending agents, sweetening, flavoring and perfuming agents, and the like.

For the preparation of fluids for parenteral administration, suitable carriers include sterile aqueous or non-aqueous solutions, suspensions, or emulsions. Examples of non-aqueous solvents or vehicles are propylene glycol, polyethylene glycol, vegetable oils, such as olive oil and corn oil, gelatin, and injectable

organic esters such as ethyl oleate. Such dosage forms may also contain adjuvants such as preserving, wetting, emulsifying, and dispersing agents. They may be sterilized, for example, by filtration through a bacteria-retaining filter, by incorporating sterilizing agents into the compositions, by irradiating the compositions, or by heating the compositions. They can also be manufactured in the form of sterile water, or some other sterile injectable medium immediately before use.

In accordance with still another embodiment of the present invention, there is provided a method for treating diabetes, said method comprising administering to a subject in need thereof an amount of a peroxisome proliferator activated receptor-gamma (PPAR-y) agonist effective to lower the blood glucose level of said subject.

As employed herein, the phrase "amount... effective to lower blood glucose levels" refers to levels of compound sufficient to provide circulating concentrations high enough to accomplish the desired effect. Such a concentration typically falls in the range of about 10 nM up to 2 μ M; with concentrations in the range of about 100 nM up to 200 nM being preferred.

The invention will now be described in greater detail by reference to the following non-limiting examples.

Example 1 Preparation of GAL4-receptor fusion proteins

A basic vector useful for the generation of GAL4-receptor fusion proteins is called pCMX-GAL4 (see SEQ ID NO:2). This vector encodes GAL4 DNA binding

domain, followed by a polylinker sequence useful in the cloning. The parental expression vector pCMX has been described by Umesono et al., in Cell 65:1255-1266 (1991), and the GAL4 portion of pCMX-GAL4 is derived from plasmid pSG424, described by Sadowski and Ptashne, in Nucleic Acids Res. 17:7539 (1989).

In general, GAL4-receptor ligand binding domain fusions are prepared by taking advantage of mutant receptor cDNA clones, such as GR-RAR chimera [see, for example, Giguere et al., in Nature 330:624-629 (1987)]. These mutant receptor cDNAs encode common XhoI sites at the end of the DNA binding domain, as described by Giguere et al., supra. To do so, a new pCMX-GAL4 vector was prepared which encodes a compatible SalI site in the polylinker sequence (there is an XhoI site in the GAL4 sequence):

SalI site: G'TCGAC
XhoI site: C'TCGAG

This allows efficient transfer of the receptor ligand
binding domain to GAL4 DNA binding domain. Through this
method, a number of chimeric species have been generated,
including GAL4-PPARy, containing residues 163-475 of
PPARy (see SEQ ID NO:1).

If mutants of the type referred to above are
not available for the construction of GAL4-containing
chimerics, one may simply look for any convenient
restriction enzyme site within or downstream of the DNA
binding domain of the receptor of interest (i.e., within
about the first 30 amino acid residues downstream of the
conserved Gly-Met residues of the DNA binding domain,
i.e., within 30 residues of the last two residues shown
in SEQ ID NO:1), and utilize the carboxy terminal
sequences therefrom.

WO 96/33724 PCT/US96/05465

23

Example 2

Preparation of reporter constructs

Various reporter constructs are used in the examples which follow. They are prepared as follows:

TK-LUC: The MTV-LTR promoter sequence was removed from the MTV-LUC plasmid described by Hollenberg and Evans in Cell 55:899-906 (1988) by HindIII and XhoI digest, and cloned with the HindIII-XhoI fragment of the Herpes simplex virus thymidine kinase gene promoter (-105 to +51 with respect to the transcription start site, m, isolated from plasmid pBLCAT2, described by Luckow & Schutz in Nucleic Acids Res. 15:5490 (1987)) to generate parental construct TK-LUC.

pTK-PPRE3-LUC: Three copies of double-stranded 15 peroxisome proliferator response element (PPRE) oligonucleotides (see SEQ ID NO:3) were cloned upstream of the TK promoter of TK-LUC at the SalI site.

pTK-MH100x4-LUC: Four copies of doublestranded MH100 oligonucleotides, encoding a GAL4 binding 20 site, were cloned upstream of the TK promoter of TK-LUC at the *Hin*dIII site.

CMX-βGAL: The coding sequence for the *E. coli* β-galactosidase gene was isolated from plasmid pCH110 [see Hall et al., J. Mol. Appl. Genet. 2:101-109 (1983)] by *HindIII* and *Bam*HI digest, and cloned into pCMX eucaryotic expression vector [see Umesono et al., supra].

Example 3

Screening assay for receptor selective agonists

CV-1 cells are co-transfected with CMX-GAL-30 PPARy and pTK-MH100x4-LUC at a ratio of about 100 ng of

receptor-encoding DNA per 10⁵ cells. The usual amounts of DNA per 10⁵ cells are 100 ng of CMX-GAL-PPARy, 300 ng of pTK-MH100x4-LUC, and 500 ng of CMX-βGAL. Typically, transfections are performed in triplicate. The plates are then incubated for 2-3 hours at 37°C.

The cells are washed with fresh medium. Fresh medium containing one concentration of a serial dilution of agonist is added to each well. A typical agonist dilution series extends from 10⁻⁵M through 10⁻¹¹M. A solvent control is performed for each agonist. The cells are incubated at 37°C for 1-2 days.

The cells are rinsed twice with buffered saline solution. Subsequently, cells are lysed, in situ, by adding 200 μ l of lysis buffer. After 30 minutes incubation at room temperature, 40 μ l aliquots of cell lysate are transferred to 96-well plates for luciferase reporter gene assays and β -galactosidase transfection controls [see Heyman et al., Cell $\underline{68}$:397-406 (1992)].

The data are expressed as relative light units (RLUs) per O.D. unit of β -galactosidase per minute. The triplicates are averaged for each concentration and plotted (see Figure 1) as fold induction induced by a standard dose (10 μ M) of agonist.

Example 4

Dose response of GAL4-PPARy constructs to various prostaglandins

Effector plasmid, reporter plasmid, and β-galactosidase control plasmid are co-transfected into CV-1 cells at a ratio of about 1:3:5, using a liposome30 mediated method, employing N-{2-(2,3)-dioleoyloxy)propylN,N,N-trimethyl ammonium methyl sulfate} (i.e., DOTAP,
Boehringer Mannheim) according to the manufacturer's

instructions in Dulbecco's modified Eagle's medium (DMEM) with 10% delipidated hormone-depleted fetal calf serum. After about 2-3 hours, the cells are washed with DMEM and an appropriate prostaglandin is added to the media to the final molar concentration indicated in Figure 2. After 24-48 hours of incubation, the cells are rinsed with phosphate buffered saline (pH 7.2) and lysed. Aliquots are assayed for luciferase and β -galactosidase activity. Luciferase activity is normalized to optical density units of β -galactosidase per minute of incubation.

The data are expressed in Figure 2 as fold induction over the same construct incubated in solvent alone. Review of Figure 2 reveals that PGD2 and PGJ2 families of compounds are functional modulators of PPARy.

While the invention has been described in detail with reference to certain preferred embodiments thereof, it will be understood that modifications and variations are within the spirit and scope of that which is described and claimed.

WO 96/33724 PCT/US96/05465

26

SEQUENCE LISTING

(1) GENERAL INFORMATION: (i) APPLICANT: Evans, Ronald M. Forman, Barry M. 5 (ii) TITLE OF INVENTION: SELECTIVE MODULATORS OF PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR-GAMMA, AND METHODS FOR THE USE THEREOF (iii) NUMBER OF SEQUENCES: 6 10 (iv) CORRESPONDENCE ADDRESS: (A) ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark(B) STREET: 444 South Flower Street, Suite 2000 (C) CITY: Los Angeles (D) STATE: CA (E) COUNTRY: USA 15 (F) ZIP: 90071 (v) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS 20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (vi) CURRENT APPLICATION DATA: (A) APPLICATION NUMBER: US 08/465,375 (B) FILING DATE: 05-JUN-1995 25 (C) CLASSIFICATION: (vii) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: US 08/428,559 (B) FILING DATE: 25-APR-1995 (viii) ATTORNEY/AGENT INFORMATION: 30 (A) NAME: Reiter, Stephen E. (B) REGISTRATION NUMBER: 31,192 (C) REFERENCE/DOCKET NUMBER: P41 90001 (ix) TELECOMMUNICATION INFORMATION: (A) TELEPHONE: 619-546-1995 35 (B) TELEFAX: 619-546-9392 (2) INFORMATION FOR SEQ ID NO:1: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2005 base pairs (B) TYPE: nucleic acid 40 (C) STRANDEDNESS: both (D) TOPOLOGY: both (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(B) LOCATION: 352..1776

(A) NAME/KEY: CDS

(ix) FEATURE:

WO 96/33724 PCT/US96/05465

										_	•						
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	GGG	ACCG.	AGT (GTGA	CGAC	AA G	GTGA	CCGG	G CT	GAGG	GGAC	GGG	CTGA	GGA	GAAG	TCACA	180
	TCT	GACA	GGA (GCCT	GTGA	GA C	CAAC	AGCC:	r GA	CGGG	GTCT	CGG	TTGA	GGG	GACG	CGGGC:	r 240
	GAG	AAGT	CAC (GTTC	TGAC	AG G	ACTG'	rg t g i	A CA	GACA	AGAT	TTG.	AAAG.	AAG	CGGT	GAACC	A 300
5	CTG	ATAT	TCA (ggac:	ATTT:	TT A	AAAA	CAAG	A CT	ACCC	TTTA	CTG	TAAA	TAC	Me	G GTT t Val 1	357
10	GAC Asp	ACA Thr	GAG Glu 5	ATG Met	CCA Pro	TTC Phe	TGG Trp	CCC Pro 10	ACC Thr	AAC Asn	TTC Phe	GGA Gly	ATC Ile 15	AGC Ser	TCT Ser	GTG Val	405
	GAC Asp	CTC Leu 20	TCC Ser	GTG Val	ATG Met	GAA Glu	GAC Asp 25	CAC His	TCG Ser	CAT His	TCC Ser	TTT Phe 30	GAC Asp	ATC Ile	AAG Lys	CCC Pro	453
15	TTT Phe 35	ACC Thr	ACA Thr	GTT Val	GAT Asp	TTC Phe 40	TCC Ser	AGC Ser	ATT Ile	TCT Ser	GCT Ala 45	CCA Pro	CAC His	TAT Tyr	GAA Glu	GAC Asp 50	501
	ATT Ile	CCA Pro	TTC Phe	ACA Thr	AGA Arg 55	GCT Ala	GAC Asp	CCA Pro	ATG Met	GTT Val 60	GCT Ala	GAT Asp	TAC Tyr	AAA Lys	TAT Tyr 65	GAC Asp	549
20	CTG Leu	AAG Lys	CTC Leu	CAA Gln 70	GAA Glu	TAC Tyr	CAA Gln	AGT Ser	GCG Ala 75	ATC Ile	AAA Lys	GTA Val	GAA Glu	CCT Pro 80	GCA Ala	TCT Ser	597
25	CCA Pro	CCT Pro	TAT Tyr 85	TAT Tyr	TCT Ser	GAA Glu	AAG Lys	ACC Thr 90	CAG Gln	CTC Leu	TAC Tyr	AAC Asn	AGG Arg 95	CCT Pro	CAT His	GAA Glu	645
	GAA Glu	CCT Pro 100	TCT Ser	AAC Asn	TCC Ser	CTC Leu	ATG Met 105	GCC Ala	ATT Ile	GAG Glu	TGC Cys	CGA Arg 110	GTC Val	TGT Cys	GGG Gly	GAT Asp	693
30	AAA Lys 115	GCA Ala	TCA Ser	GGC Gly	TTC Phe	CAC His 120	TAT Tyr	GGA Gly	GTT Val	CAT His	GCT Ala 125	TGT Cys	GAA Glu	GGA Gly	TGC Cys	AAG Lys 130	741
	GGT Gly	TTT Phe	TTC Phe	CGA Arg	AGA Arg 135	ACC Thr	ATC Ile	CGA Arg	TTG Leu	AAG Lys 140	CTT Leu	ATT Ile	TAT Tyr	GAT Asp	AGG Arg 145	TGT Cys	789
35	GAT Asp	CTT Leu	AAC Asn	TGC Cys 150	CGG Arg	ATC Ile	CAC His	AAA Lys	AAA Lys 155	AGT Ser	AGA Arg	AAT Asn	AAA Lys	TGT Cys 160	CAG Gln	TAC Tyr	837
40	Cys	CGG Arg	TTT Phe 165	CAG Gln	AAG Lys	TGC Cys	CTT Leu	GCT Ala 170	GTG Val	GGG Gly	ATG Met	TCT Ser	CAC His 175	AAT Asn	GCC Ala	ATC Ile	885
	AGG Arg	TTT Phe 180	GGG Gly	CGG Arg	ATG Met	CCA Pro	CAG Gln 185	GCC Ala	GAG Glu	AAG Lys	GAG Glu	AAG Lys 190	CTG Leu	TTG Leu	GCG Ala	GAG Glu	933
45	ATC Ile 195	TCC Ser	AGT Ser	GAT Asp	ATC Ile	GAC Asp 200	CAG Gln	CTG Leu	AAC Asn	CCA Pro	GAG Glu 205	TCT Ser	GCT Ala	GAT Asp	CTG Leu	CGA Arg 210	981
	GCC Ala	CTG Leu	GCA Ala	AAG Lys	CAT His 215	TTG Leu	TAT Tyr	GAC Asp	TCA Ser	TAC Tyr 220	ATA Ile	AAG Lys	TCC Ser	TTC Phe	CCG Pro 225	CTG Leu	1029

	ACC Thr	AAA Lys	GCC Ala	AAG Lys 230	Ala	AGG Arg	GCG Ala	ATC	1 TTC Leu 235	Thr	GG/	A AAG	ACA Thr	ACG Thr 240	Asp	AAA Lys	1077
5	TCA Ser	CCA Pro	TTT Phe 245	GTC Val	ATC Ile	TAC Tyr	GAC Asp	ATG Met 250	Asn	TCC Ser	TTA Leu	ATG Met	ATG Met	Gly	GAA Glu	GAT Asp	1125
	AAA Lys	ATC Ile 260	rys	TTC Phe	AAA Lys	CAT His	ATC Ile 265	Thr	CCC	CTG Leu	CAG Gln	GAG Glu 270	Gln	AGC Ser	AAA Lys	GAG Glu	1173
10	GTG Val 275	WIG	ATC Ile	CGA Arg	ATT Ile	TTT Phe 280	GIn	GGG Gly	TGC Cys	CAG Gln	TTT Phe 285	Arg	TCC	GTA Val	GAA Glu	GCC Ala 290	1221
15	GTG Val	CAA Gln	GAG Glu	ATC Ile	ACA Thr 295	GAG Glu	TAT Tyr	GCC Ala	AAA Lys	AAT Asn 300	ATC Ile	CCT Pro	GGT Gly	TTC Phe	ATT Ile 305	AAC Asn	1269
	CTT Leu	GAT Asp	TTG Leu	AAT Asn 310	GAC	CAA Gln	GTG Val	ACT Thr	CTG Leu 315	CTC Leu	AAG Lys	TAT Tyr	GGT Gly	GTC Val 320	CAT His	GAG Glu	1317
20	ATC Ile	ATC Ile	TAC Tyr 325	ACG Thr	ATG Met	CTG Leu	GCC Ala	TCC Ser 330	CTG Leu	ATG Met	AAT Asn	AAA Lys	GAT Asp 335	GGA Gly	GTC Val	CTC Leu	1365
	ATC Ile	TCA Ser 340	GAG Glu	GGC Gly	CAA Gln	GGA Gly	TTC Phe 345	ATG Met	ACC Thr	AGG Arg	GAG Glu	TTC Phe 350	CTC Leu	AAA Lys	AGC Ser	CTG Leu	1413
25	CGG Arg 355	AAG Lys	CCC Pro	TTT Phe	GGT Gly	GAC Asp 360	TTT Phe	ATG Met	GAG Glu	CCT Pro	AAG Lys 365	TTT Phe	GAG Glu	TTT Phe	GCT Ala	GTG Val 370	1461
30	AAG Lys	TTC Phe	AAT Asn	GCA Ala	CTG Leu 375	GAA Glu	TTA Leu	GAT Asp	GAC Asp	AGT Ser 380	GAC Asp	TTG Leu	GCT Ala	ATA Ile	TTT Phe 385	ATA Ile	1509
	GCT Ala	GTC Val	ATT Ile	ATT Ile 390	CTC Leu	AGT Ser	GGA Gly	GAC Asp	CGC Arg 395	CCA Pro	GGC Gly	TTG Leu	CTG Leu	AAC Asn 400	GTG Val	AA G Lys	1557
35	CCC Pro	ATC Ile	GAG Glu 405	GAC Asp	ATC Ile	CAA Gln	GAC Asp	AAC Asn 410	CTG Leu	CTG Leu	CAG Gln	GCC Ala	CTG Leu 415	GAA Glu	CTG Leu	CAG Gln	1605
	CTC Leu	AAG Lys 420	CTG Leu	AAT Asn	CAC His	CCA Pro	GAG Glu 425	TCC Ser	TCT Ser	CAG Gln	CTG Leu	TTC Phe 430	GCC Ala	A AG Lys	GTG Val	CTC Leu	1653
40	CAG Gln 435	AAG Lys	ATG Met	ACA Thr	GAC Asp	CTC Leu 440	AGG Arg	CAG Gln	ATC Ile	GTC Val	ACA Thr 445	GAG Glu	CAC His	GTG Val	Gln :	CTA Leu 450	1701
45	CTG Leu	CAT His	GTG Val	Ile	AAG Lys 455	AAG Lys	ACA Thr	GAG Glu	Thr	GAC Asp 460	ATG Met	AGC Ser	CTT Leu	His	CCC (Pro 1 465	CTG Leu	1749
	CTC Leu	CAG Gln	Glu	ATC Ile 470	TAC Tyr	AA G Lys	GAC Asp	Leu	TAT Tyr 475	TAGC	AGGA	AA G	TCCC.	ACCC	G		1796
	CTGA	CAAC	GT G	TTCC	TTCT	A TT	GATT	GCAC	TAT	TATT	TTG	AGGG	AAAA	AA A	rctg;	ACACC	1856

WO 96/33724 PCT/US96/05465

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	ATG	CATA	TTG	TTTA	AAAT	GA T	ACAT	TTAC	A AI	TTAC	TTTI	CAA ?	ATTA	AAA	ATTA	CCACAT	1	976
	TAT	'AAAA	AAA	AAAA	AAAA	AA A	GGAA	TTCC	!								2	2005
	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 2	:									
5		(i	(A) L B) T C) S	CE C ENGT YPE: TRAN OPOL	H: 5 nuc DEDN	46 b leic ESS:	ase aci bot	pair d	s								
10		(ii) MO	LECU	LE T	YPE:	CDN	A										
		(ix	(E: AME/: OCAT													
		(xi) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:2:							
15	GGG.	AGAC	CCA .	AGCT	TGAA	GC A	AGCC'	TCCT	G AA		TG A et L 1							52
20	ATC Ile	GAA Glu	CAA Gln	GCA Ala 10	TGC Cys	GAT	ATT Ile	TGC Cys	CGA Arg 15	CTT Leu	AAA Lys	AAG Lys	CTC Leu	AAG Lys 20	Cys	TCC Ser		100
	AAA Lys	GAA Glu	AAA Lys 25	CCG Pro	AAG Lys	TGC Cys	GCC Ala	AAG Lys 30	TGT Cys	CTG Leu	AAG Lys	AAC Asn	AAC Asn 35	TGG Trp	GAG Glu	TGT Cys		148
25	CGC Arg	TAC Tyr 40	TCT Ser	CCC Pro	AAA Lys	ACC Thr	AAA Lys 45	AGG Arg	TCT Ser	CCG Pro	CTG Leu	ACT Thr 50	AGG Arg	GCA Ala	CAT His	CTG Leu	;	196
	ACA Thr 55	GAA Glu	GTG Val	GAA Glu	TCA Ser	AGG Arg 60	CTA Leu	GAA Glu	AGA Arg	CTG Leu	GAA Glu 65	CAG Gln	CTA Leu	TTT Phe	CTA Leu	CTG Leu 70	:	244
30	ATT Ile	TTT Phe	CCT	CGA Arg	GAA Glu 75	GAC Asp	CTT Leu	GAC Asp	ATC Met	ATT Lle 80	TTG Leu	AAA Lys	ATG Met	GAT Asp	TCT Ser 85	TTA Leu	2	292
35	CAG Gln	GAT Asp	ATA Ile	AAA Lys 90	GCA Ala	TTG Leu	TTA Leu	ACA Thr	GGA Gly 95	TTA Leu	TTT Phe	GTA Val	CAA Gln	GAT Asp 100	AAT Asn	GTG Val	3	340
	AAT Asn	AAA Lys	GAT Asp 105	GCC Ala	GTC Val	ACA Thr	GAT Asp	AGA Arg 110	TTG Leu	GCT Ala	TCA Ser	GTG Val	GAG Glu 115	ACT Thr	GAT Asp	ATG Met	3	888
40	CCT Pro	CTA Leu 120	ACA Thr	TTG Leu	AGA Arg	CAG Gln	CAT His 125	AGA Arg	ATA Ile	AGT Ser	GCG Ala	ACA Thr 130	TCA Ser	TCA Ser	TCG Ser	GAA Glu	4	136
	GAG Glu 135	AGT Ser	AGT Ser	AAC Asn	Lys	GGT Gly 140	CAA Gln	AGA Arg	CAG Gln	TTG Leu	ACT Thr 145	GTA Val	TCG Ser	CCG Pro	GAA Glu	TTC Phe 150	4	184
45	CCG Pro	GGG Gly	ATC Ile	CGT Arg	CGA Arg 155	CGG Arg	TAC Tyr	CAG Gln	ATA Ile	TCA Ser 160	GGA Gly	TCC Ser	TGG Trp	CCA Pro	GCT Ala 165	AGC Ser	5	32

WO 96/33724 PCT/US96/05465

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TAG GTA GCT AGA GG
* Val Ala Arg
170

5

546

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu

1 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu 20 25 30

15 Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile 20 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu 85 90 95

Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
100 105 110

25 Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser 115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu 130 135 140

Thr Val Ser Pro Glu Phe Pro Gly Ile Arg Arg Tyr Gln Ile Ser 30 145 150 155 160

Gly Ser Trp Pro Ala Ser * Val Ala Arg

- (2) INFORMATION FOR SEQ ID NO:4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both
 - (ii) MOLECULE TYPE: DNA (genomic)
- 40 (xi) SEQUENCE DESCRIPTION: SEO ID NO:4:

AGGACAAAGG TCA

WO 96/33724	PCT/US96/0546
	101/0

(2)	INFORMATION	FOR	SEQ	ID	NO:5:
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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGACCAGGAC AAAGGTCACG TTC

5

23

- 10 (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both
- 15 (D) TOPOLOGY: both
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGAGGACTG TCCTCCG

That which is claimed is:

- A method for modulating process(es) mediated by peroxisome proliferator activated receptor-gamma (PPAR-y), said method comprising conducting said process(es) in the presence of at least one PPAR-y-selective prostaglandin or prostaglandin-like compound or precursor thereof.
 - 2. A method according to Claim 1 wherein said PPAR-y-selective prostaglandin is selected from a prostaglandin- J_2 , a prostaglandin- D_2 , or a precursor thereof.
 - 3. A method according to Claim 2 wherein said prostaglandin-J₂ is selected from prostaglandin-J₂, $\Delta^{12}\text{-prostaglandin-J}_2 \text{ or } 15\text{-deoxy-}\Delta^{12,14}\text{-prostaglandin-J}_2.$
 - 4. A method according to Claim 1, wherein said-PPAR-y-selective prostaglandin or prostaglandin-like compound has the structure I:

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wherein:

A is selected from hydrogen or a leaving group at the α - or β - position of the ring, or A is absent when there is a double bond between C^{α} and C^{β} of the ring;

15

X is an alkyl, substituted alkyl, alkenyl, substituted alkenyl, alkynyl or

substituted alkynyl group having in the range of 2 up to 15 carbon atoms; and

Y is an alkyl, substituted alkyl, alkenyl, substituted alkenyl, alkynyl or substituted alkynyl group having in the range of 2 up to 15 carbon atoms.

5. A method according to claim 4 wherein:

X of Formula I is selected from: $-(CRR)_{m}-Z$, $-(CRR)_{m'}-C(R)=C(R)-(CRR)_{m'}-Z$, or 5 -(CRR)_{m"}-C \equiv C-(CRR)_{m"}-Z, wherein: each R is independently selected from hydrogen, lower alkyl, substituted lower alkyl, hydroxy, lower alkoxy, thioalkyl, halogen, trifluoromethyl, 10 cyano, nitro, amino, carboxyl, carbamate, sulfonyl or sulfonamide, m falls in the range of 1 up to 15, each m' falls independently in the range of 0 up to 12, with the proviso that 15 the total chain length of the alkenyl moiety does not exceed 15 carbon

atoms,

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each m" falls independently in the range of 0 up to 12, with the proviso that the total chain length of the alkynyl moiety does not exceed 15 carbon atoms, and

Z is a polar, heteroatom-containing substituent; and

25	Y of Formula I is selected from: $=C(R)-[C(R)=C(R)]_{n}-(CRR)_{n},-Z' (II),$ $=C(R)-[C=C]_{n}-(CRR)_{n},-Z' (IIA),$ $=C(R)-CRR-CR(R)_{n}-CRR_{n}-CR$
	$=C(R)-CRR-CR(R')-(CRR)_{n'}-Z' (III),$
30	$-[C(R)=C(R)]_{n}-(CRR)_{n'}-Z' (IV),$
30	-[C≡C] _n -(CRR) _n ,-Z' (IVA), wherein
	each R is independently as defined
	above,
	each R' is independently selected
35	from H, lower alkyl, substituted
	lower alkyl, or a leaving group,
	Z' is selected from H, lower alkyl or
	substituted lower alkyl,
	n falls in the range of 0 up to 4,
40	n' falls in the range of 2 up to 12, and
	n" falls in the range of 1 up to 3.
	•
	6. A method according to claim 5 wherein Z is
	6. A method according to claim 5 wherein Z is selected from cyano, nitro, amino, carbamate, or a
	selected from cyano, nitro, amino, carbamate, or a
5	selected from cyano, nitro, amino, carbamate, or a substituent having the structure:
5	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH ₂ OR', wherein R' is selected from H, alkyl,
5	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH ₂ OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl;
5	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH ₂ OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl,
5	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino,</pre>
5	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH₂OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl,</pre>
	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted
	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl,</pre>
	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted aryl, aryloxy, arylamino, alkylaryl, substituted alkylaryl, arylalkyl,</pre>
	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted aryl, aryloxy, arylamino, alkylaryl, substituted alkylaryl, arylalkyl, substituted arylalkyl, heterocyclic, substituted heterocyclic or trifluoromethyl,</pre>
	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted aryl, aryloxy, arylamino, alkylaryl, substituted alkylaryl, arylalkyl, substituted arylalkyl, heterocyclic, substituted heterocyclic or
10	<pre>selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl,</pre>
10	selected from cyano, nitro, amino, carbamate, or a substituent having the structure: -CH2OR', wherein R' is selected from H, alkyl, alkenyl, alkynyl, acyl or aryl; -C(O)R", wherein R" is selected from H, alkyl, substituted alkyl, alkoxy, alkylamino, alkenyl, substituted alkenyl, alkynyl, substituted alkynyl, aryl, substituted aryl, aryloxy, arylamino, alkylaryl, substituted alkylaryl, arylalkyl, substituted alkylaryl, arylalkyl, substituted arylalkyl, heterocyclic, substituted heterocyclic or trifluoromethyl, -CO2R''', wherein R''' is selected from H,

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7.	Α	method	according	to	claim	5	wherein:
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Х	of	Formula	I	is	$-CRR-C(R)=C(R)-(CRR)_m-Z$,
		wherein	:		

each R is independently selected from hydrogen, lower alkyl, substituted lower alkyl, hydroxy, alkoxy (of a lower alkyl group), halogen, trifluoromethyl, amino, carboxyl, or sulfonyl,

m falls in the range of 1 up to 6, and Z is selected from -CH₂OH, -CH₂OAc, -CO₂H, -CO₂Me or -CO₂Et; and

Y of Formula I is selected from:

 $=C(R)-C(R)=C(R)-(CRR)_{n'}-Z'$ (II),

 $=C(R)-CRR-CR(R')-(CRR)_{n'}-Z'$ (III), or

-C(R)=C(R)-CR(R')-(CRR)_{n'}-Z' (IV), wherein each R is independently as defined above,

each R' is independently selected
from H, lower alkyl, substituted
lower alkyl, or a leaving group,
Z' is selected from H, lower alkyl or
substituted lower alkyl, and
n' falls in the range of 1 up to 6.

8. A method according to claim 7 wherein Y of Formula I is

$$=C(R)-C(R)=C(R)-(CRR)_{p},-Z'$$
 (II),

wherein each R is selected from hydrogen, lower alkyl or substituted lower alkyl, n is 1, n' falls in the range of about 2 up to 6, and Z' is selected from hydrogen or lower alkyl.

9. A method according to claim 7 wherein Y of Formula ${\bf I}$ is

- wherein each R is selected from hydrogen, lower alkyl or substituted lower alkyl, R' is selected from hydrogen, lower alkyl, or an hydroxy group, n is 1, n' falls in the range of about 2 up to 6, and Z' is selected from hydrogen or lower alkyl.
 - 10. A method according to claim 5 wherein A is 9-OH, Y is IV, each R is hydrogen, R' is hydroxy, Z is $-CO_2H$, m=3, Z' is methyl, n=1 and n'=4.
 - 11. A method according to claim 5 wherein A is absent, Y is IV, each R is hydrogen, R' is hydroxy, Z is $-CO_2H$, m is 3, Z' is methyl, n=1 and n'=4.
 - 12. A method according to claim 5 wherein A is absent, Y is II, each R is hydrogen, R' is hydroxy, Z is $-CO_2H$, m=3, Z' is methyl, n=1 and n'=4.
 - 13. A method according to claim 5 wherein A is absent, Y is I, each R is hydrogen, Z is $-CO_2H$, m=3, Z' is methyl, n=1 and n'=4.
 - 14. A method according to claim 1 wherein said process mediated by PPAR-y is cell differentiation to produce lipid-accumulating cells.
 - 15. A method according to claim 1 wherein said process mediated by PPAR- γ is the response of the recipient to insulin.

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37

ability to regulate transcription-activating effects of a peroxisome proliferator activated receptor-gamma (PPAR-y), said method comprising assaying for changes in the level of reporter protein present as a result of contacting cells containing said receptor and reporter vector with said compound;

wherein said reporter vector comprises:

- (a) a promoter that is operable in said cell,
- (b) a hormone response element, and
- (c) a DNA segment encoding a reporter protein,

wherein said reporter proteinencoding DNA segment is operatively linked to said promoter for transcription of said DNA segment, and

wherein said hormone response element is operatively linked to said promoter for activation thereof.

17. A method according to Claim 16 wherein said hormone response element is a direct repeat of two or more half sites separated by a spacer of one nucleotide, wherein said spacer can be A, C, G or T, wherein each half site comprises the sequence -RGBNNM-,

wherein

R is selected from A or G;
B is selected from G, C, or T;
each N is independently selected from
A, T, C, or G; and

M is selected from A or C;

with the proviso that at least 4 nucleotides of said -RGBNNM- sequence are identical with the nucleotides at corresponding positions of the sequence -AGGTCA-; and

wherein said response element is optionally preceded by N_x , wherein x falls in the range of 0 up to 5.

18. A method according to claim 17 wherein said response element has at least one copy of the minimal sequence:

AGGACA A AGGTCA,

- 5 wherein said minimal sequence is optionally flanked by additional residues.
 - 19. A method according to claim 17 wherein said response element has at least one copy of the sequence:

GGACC AGGACA A AGGTCA CGTTC.

- 20. A method according to claim 16 wherein said compound is a putative antagonist for said peroxisome proliferator activated receptor-gamma, and wherein said contacting is carried out in the presence of
- increasing concentrations of said compound, and

- a fixed concentration of at least one agonist for said peroxisome proliferator activated receptor-gamma.
- 21. A method according to Claim 16 wherein said contacting is carried out in the further presence of at least one PPAR-y-selective modulator.
- 22. A method for preventing obesity, said method comprising administering to a subject in need thereof an amount of a peroxisome proliferator activated receptor-gamma (PPAR-y) antagonist effective to block cell differentiation to produce lipid-accumulating cells.

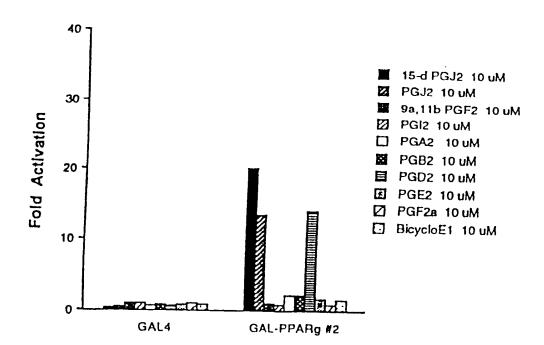
WO 96/33724 PCT/US96/05465

39

23. A method for treating diabetes, said method comprising administering to a subject in need thereof an amount of a peroxisome proliferator activated receptor-gamma (PPAR-y) agonist effective to lower the blood glucose level of said subject.

1/2

FIGURE 1



WO 96/33724

PCT/US96/05465

2/2

FIGURE 2

Activation of PPARy by Prostaglandins

